



SEQUENCE LISTING

<110> Chou, Min-Yuan
Leu, Charng-Yih

<120> Novel Human alpha 1 Chain Collagen

<130> 32350-176844

<140> US 09/996,611

<141> 2001-11-30

<150> Taiwan 89128027

<151> 2000-12-27

<160> 15

<170> PatentIn version 3.2

<210> 1

<211> 954

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala His Tyr Ile Thr Phe Leu Cys Met Val Leu Val Leu Leu Leu
1 5 10 15

Gln Asn Ser Val Leu Ala Glu Asp Gly Glu Val Arg Ser Ser Cys Arg
20 25 30

Thr Ala Pro Thr Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser Val
35 40 45

Gly Pro Glu Asn Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile Thr
50 55 60

Lys Asn Phe Asp Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val Gln
65 70 75 80

Tyr Ser Asp Tyr Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp Ser
85 90 95

Gly Glu His Leu Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly Gly
100 105 110

Asn Thr Lys Thr Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr Leu Phe
115 120 125

Ala Lys Ser Ser Arg Phe Leu Thr Lys Ile Ala Val Val Leu Thr Asp
130 135 140

Gly Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln Ala Ala Arg Asp
145 150 155 160

Ser Lys Ile Thr Leu Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp
 165 170 175

Ala Glu Leu Arg Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe
 180 185 190

Tyr Val Glu Asp Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met Lys
 195 200 205

Gln Lys Leu Cys Glu Glu Ser Val Cys Pro Thr Arg Ile Pro Val Ala
 210 215 220

Ala Arg Asp Glu Arg Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn
 225 230 235 240

Lys Lys Val Lys Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys Gly
 245 250 255

Tyr Glu Val Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser Asn Val
 260 265 270

Phe Pro Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser Thr Gln Arg
 275 280 285

Phe Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile Asp
 290 295 300

Gly Arg Pro Gln Ile Ala Val Thr Leu Asn Gly Val Asp Lys Ile Leu
 305 310 315 320

Leu Phe Thr Thr Thr Ser Val Ile Asn Gly Ser Gln Val Val Thr Phe
 325 330 335

Ala Asn Pro Gln Val Lys Thr Leu Phe Asp Glu Gly Trp His Gln Ile
 340 345 350

Arg Leu Leu Val Thr Glu Gln Asp Val Thr Leu Tyr Ile Asp Asp Gln
 355 360 365

Gln Ile Glu Asn Lys Pro Leu His Pro Val Leu Gly Ile Leu Ile Asn
 370 375 380

Gly Gln Thr Gln Ile Gly Lys Tyr Ser Gly Lys Glu Glu Thr Val Gln
 385 390 395 400

Phe Asp Val Gln Lys Leu Arg Ile Tyr Cys Asp Pro Glu Gln Asn Asn
 405 410 415

Arg Glu Thr Ala Cys Glu Ile Pro Gly Phe Cys Leu Asn Gly Pro Ser
 420 425 430

Asp Val Gly Ser Thr Pro Ala Pro Cys Ile Cys Pro Pro Gly Lys Pro
 435 440 445

Gly Leu Gln Gly Pro Lys Gly Asp Pro Gly Leu Pro Gly Asn Pro Gly
 450 455 460

Tyr Pro Gly Gln Pro Gly Gln Asp Gly Lys Pro Gly Tyr Gln Gly Ile
 465 470 475 480

Ala Gly Thr Pro Gly Val Pro Gly Ser Pro Gly Ile Gln Gly Ala Arg
 485 490 495

Gly Leu Pro Gly Tyr Lys Gly Glu Pro Gly Arg Asp Gly Asp Lys Gly
 500 505 510

Asp Arg Gly Leu Pro Gly Phe Pro Gly Leu His Gly Met Pro Gly Ser
 515 520 525

Lys Gly Glu Met Gly Ala Lys Gly Asp Lys Gly Ser Pro Gly Phe Tyr
 530 535 540

Gly Lys Lys Gly Ala Lys Gly Glu Lys Gly Asn Ala Gly Phe Pro Gly
 545 550 555 560

Leu Pro Gly Pro Ala Gly Glu Pro Gly Arg His Gly Lys Asp Gly Leu
 565 570 575

Met Gly Ser Pro Gly Phe Lys Gly Glu Ala Gly Ser Pro Gly Ala Pro
 580 585 590

Gly Gln Asp Gly Thr Arg Gly Glu Pro Gly Ile Pro Gly Phe Pro Gly
 595 600 605

Asn Arg Gly Leu Met Gly Gln Lys Gly Glu Ile Gly Pro Pro Gly Gln
 610 615 620

Gln Gly Lys Lys Gly Ala Pro Gly Met Pro Gly Leu Met Gly Ser Asn
 625 630 635 640

Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys Gly
 645 650 655

Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser Gly Leu Lys Gly Glu
 660 665 670

Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met Gly Leu Pro

675					680					685					
Gly	Ile	Gln	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Asn	Gln	Gly	Glu	Lys	Gly
690						695					700				
Ile	Gln	Gly	Gln	Lys	Gly	Glu	Asn	Gly	Arg	Gln	Gly	Ile	Pro	Gly	Gln
705					710					715					720
Gln	Gly	Ile	Gln	Gly	His	His	Gly	Ala	Lys	Gly	Glu	Arg	Gly	Glu	Lys
				725					730					735	
Gly	Glu	Pro	Gly	Val	Arg	Gly	Ala	Ile	Gly	Ser	Lys	Gly	Glu	Ser	Gly
			740					745					750		
Val	Asp	Gly	Leu	Met	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Gln	Pro	Gly	Asp
		755					760					765			
Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Leu	Asp	Gly	Lys	Pro	Gly	Arg	Glu
	770					775					780				
Phe	Ser	Glu	Gln	Phe	Ile	Arg	Gln	Val	Cys	Thr	Asp	Val	Ile	Arg	Ala
785					790					795					800
Gln	Leu	Pro	Val	Leu	Leu	Gln	Ser	Gly	Arg	Ile	Arg	Asn	Cys	Asp	His
				805					810					815	
Cys	Leu	Ser	Gln	His	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Pro	Pro	Gly	Pro
			820					825					830		
Ile	Gly	Pro	Glu	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Leu	Pro	Gly	Arg	Asp
	835						840					845			
Gly	Val	Pro	Gly	Leu	Val	Gly	Val	Pro	Gly	Arg	Pro	Gly	Val	Arg	Gly
	850					855					860				
Leu	Lys	Gly	Leu	Pro	Gly	Arg	Asn	Gly	Glu	Lys	Gly	Ser	Gln	Gly	Phe
865					870					875					880
Gly	Tyr	Pro	Gly	Glu	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Glu	Gly
				885					890					895	
Pro	Pro	Gly	Ile	Ser	Lys	Glu	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Leu	Pro
			900					905					910		
Gly	Lys	Asp	Gly	Asp	His	Gly	Lys	Pro	Gly	Ile	Gln	Gly	Gln	Pro	Gly
		915					920					925			
Pro	Pro	Gly	Ile	Cys	Asp	Pro	Ser	Leu	Cys	Phe	Ser	Val	Ile	Ala	Arg
		930				935					940				

Arg Asp Pro Phe Arg Lys Gly Pro Asn Tyr
945 950

<210> 2
<211> 171
<212> PRT
<213> Homo sapiens

<400> 2

Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser Val Gly Pro Glu Asn
1 5 10 15

Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile Thr Lys Asn Phe Asp
20 25 30

Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val Gln Tyr Ser Asp Tyr
35 40 45

Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp Ser Gly Glu His Leu
50 55 60

Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly Gly Asn Thr Lys Thr
65 70 75 80

Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr Leu Phe Ala Lys Ser Ser
85 90 95

Arg Phe Leu Thr Lys Ile Ala Val Val Leu Thr Asp Gly Lys Ser Gln
100 105 110

Asp Asp Val Lys Asp Ala Ala Gln Ala Ala Arg Asp Ser Lys Ile Thr
115 120 125

Leu Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp Ala Glu Leu Arg
130 135 140

Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe Tyr Val Glu Asp
145 150 155 160

Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met
165 170

<210> 3
<211> 183
<212> PRT
<213> Homo sapiens

<400> 3

Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn Lys Lys Val Lys Lys

1	5	10	15
Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys Gly Tyr Glu Val Thr Ser	20	25	30
Lys Val Asp Leu Ser Glu Leu Thr Ser Asn Val Phe Pro Glu Gly Leu	35	40	45
Pro Pro Ser Tyr Val Phe Val Ser Thr Gln Arg Phe Lys Val Lys Lys	50	55	60
Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile Asp Gly Arg Pro Gln Ile	65	70	75
Ala Val Thr Leu Asn Gly Val Asp Lys Ile Leu Leu Phe Thr Thr Thr	85	90	95
Ser Val Ile Asn Gly Ser Gln Val Val Thr Phe Ala Asn Pro Gln Val	100	105	110
Lys Thr Leu Phe Asp Glu Gly Trp His Gln Ile Arg Leu Leu Val Thr	115	120	125
Glu Gln Asp Val Thr Leu Tyr Ile Asp Asp Gln Gln Ile Glu Asn Lys	130	135	140
Pro Leu His Pro Val Leu Gly Ile Leu Ile Asn Gly Gln Thr Gln Ile	145	150	155
Gly Lys Tyr Ser Gly Lys Glu Glu Thr Val Gln Phe Asp Val Gln Lys	165	170	175
Leu Arg Ile Tyr Cys Asp Pro	180		

<210> 4
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 4

Gly Lys Pro Gly Leu Gln Gly Pro Lys Gly Asp Pro Gly Leu Pro Gly	5	10	15
Asn Pro Gly Tyr Pro Gly Gln Pro Gly Gln Asp Gly Lys Pro Gly Tyr	20	25	30
Gln Gly Ile Ala Gly Thr Pro Gly Val Pro Gly Ser Pro Gly Ile Gln	35	40	45

Gly Ala Arg Gly Leu Pro Gly Tyr Lys Gly Glu Pro Gly Arg Asp Gly
 50 55 60

Asp Lys Gly Asp Arg Gly Leu Pro Gly Phe Pro Gly Leu His Gly Met
 65 70 75 80

Pro Gly Ser Lys Gly Glu Met Gly Ala Lys Gly Asp Lys Gly Ser Pro
 85 90 95

Gly Phe Tyr Gly Lys Lys Gly Ala Lys Gly Glu Lys Gly Asn Ala Gly
 100 105 110

Phe Pro Gly Leu Pro Gly Pro Ala Gly Glu Pro Gly Arg His Gly Lys
 115 120 125

Asp Gly Leu Met Gly Ser Pro Gly Phe Lys Gly Glu Ala Gly Ser Pro
 130 135 140

Gly Ala Pro Gly Gln Asp Gly Thr Arg Gly Glu Pro Gly Ile Pro Gly
 145 150 155 160

Phe Pro Gly Asn Arg Gly Leu Met Gly Gln Lys Gly Glu Ile Gly Pro
 165 170 175

Pro Gly Gln Gln Gly Lys Lys Gly Ala Pro Gly Met Pro Gly Leu Met
 180 185 190

Gly Ser Asn Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly
 195 200 205

Ser Lys Gly Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser Gly Leu
 210 215 220

Lys Gly Glu Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met
 225 230 235 240

Gly Leu Pro Gly Ile Gln Gly Lys Lys Gly Asp Lys Gly Asn Gln Gly
 245 250 255

Glu Lys Gly Ile Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln Gly Ile
 260 265 270

Pro Gly Gln Gln Gly Ile Gln Gly His His Gly Ala Lys Gly Glu Arg
 275 280 285

Gly Glu Lys Gly Glu Pro Gly Val Arg Gly Ala Ile Gly Ser Lys Gly
 290 295 300

Glu Ser Gly Val Asp Gly Leu Met Gly Pro Ala Gly Pro Lys Gly Gln
 305 310 315 320

Pro Gly Asp Pro Gly Pro Gln Gly Pro Pro Gly Leu Asp Gly Lys Pro
 325 330 335

Gly Arg Glu Phe Ser Glu Gln Phe Ile Arg Gln Val Cys Thr Asp Val
 340 345 350

Ile Arg Ala Gln Leu Pro Val Leu Leu Gln Ser Gly Arg Ile Arg Asn
 355 360 365

Cys Asp His Cys Leu Ser Gln His Gly Ser Pro Gly Ile Pro Gly Pro
 370 375 380

Pro Gly Pro Ile Gly Pro Glu Gly Pro Arg Gly Leu Pro Gly Leu Pro
 385 390 395 400

Gly Arg Asp Gly Val Pro Gly Leu Val Gly Val Pro Gly Arg Pro Gly
 405 410 415

Val Arg Gly Leu Lys Gly Leu Pro Gly Arg Asn Gly Glu Lys Gly Ser
 420 425 430

Gln Gly Phe Gly Tyr Pro Gly Glu Gln Gly Pro Pro Gly Pro Pro Gly
 435 440 445

Pro Glu Gly Pro Pro Gly Ile Ser Lys Glu Gly Pro Pro Gly Asp Pro
 450 455 460

Gly Leu Pro Gly Lys Asp Gly Asp His Gly Lys Pro Gly Ile Gln Gly
 465 470 475 480

Gln Pro Gly Pro Pro Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser Val
 485 490 495

Ile Ala Arg Arg Asp Pro Phe Arg Lys Gly Pro Asn Tyr
 500 505

<210> 5
 <211> 2865
 <212> DNA
 <213> Homo sapiens

<400> 5
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 atcttagatg gctcttatag tgttggccca gaaaactttg aaatagtgaa aaagtggcctt 180

gtcaatatca	caaaaaactt	tgacataggg	ccgaagttaa	ttcaagttgg	agtggttcaa	240
tatagtgact	accctgtgct	ggagattcct	ctcggaagct	atgattcagg	agaacatttg	300
acggcagcag	tggaatccat	actctactta	ggaggaaaca	caaagacagg	gaaggccatc	360
cagtttgccg	tcgattacct	ttttgccaaag	tcctcacgat	ttctgactaa	gatagcagtg	420
gtacttacgg	atggcaaatac	ccaagatgac	gtcaaggatg	cagctcaagc	agcaagagat	480
agtaagataa	cattatattgc	tattggtggt	ggttcagaaa	cagaagatgc	cgaacttaga	540
gctattgccca	acaagccttc	gtctacttat	gtgttttatg	tggaagacta	tattgcaata	600
tccaaaataa	gggaagtgat	gaagcagaaa	ctttgtgaag	aatctgtctg	tccaacacga	660
attccagtg	cagctcgtga	tgaaagggga	tttgatattc	ttttaggttt	agatgtaaata	720
aaaaaggtta	agaaaagaat	acagctttca	ccaaaaaaga	taaaaggata	tgaagtaaca	780
tcaaaagttg	atztatcaga	actcacaagc	aatgttttcc	cagaaggctc	tcctccatca	840
tatgtatttg	tgtctactca	aagatttaaa	gtcaagaaaa	tttgggattt	atggagaata	900
ttaactattg	atggaaggcc	acaaatagca	gttaccttaa	atggtgtgga	caaaatctta	960
ttattttaca	caaccagcgt	aattaatggc	tcacaagtgg	ttacctttgc	taaccctcaa	1020
gttaagacgt	tgtttgatga	aggctggcac	caaattcgtc	tccttagtaac	agaacaagat	1080
gtgactttgt	atattgatga	ccaacaaatt	gaaaacaagc	ccttacatcc	agtttttaggg	1140
atcttgatca	atgggcaaac	ccaaattgga	aaatattctg	gaaaagaaga	aactgttcag	1200
tttgatgtcc	aaaagttgcg	aatctactgt	gaccagaac	agaacaaccg	ggagacagca	1260
tgtgagattc	ctggattttg	ccttaatggt	cccagtgatg	taggttcaac	tccagctccc	1320
tgtatttgtc	ctccgggaaa	accaggactt	caaggcccca	aaggtagacc	tggactgcct	1380
gggaaccctg	gctaccctgg	acaacctggt	caagatggta	agcctggata	tcaggggaatt	1440
gcagggacac	caggtgttcc	aggatctcca	ggaatacaag	gagctcgagg	actaccaggt	1500
tacaaaggag	aaccagggcg	agatggtgac	aagggtgatc	gtggacttcc	tggttttcct	1560
gggcttcatg	gcatgccagg	atcaaagggg	gaaatgggtg	ccaaaggaga	caaaggatca	1620
cctggatttt	atggcaaaaa	gggtgcaaaa	ggtgaaaagg	ggaatgctgg	cttcctgggc	1680
ctccctggac	ctgctggaga	accaggaaga	catggaaaagg	atggattaat	gggtagtccc	1740
ggtttcaagg	gagaagcagg	atcccctggt	gctccggggc	aggatggaac	acggggagag	1800
cctggaatcc	caggatttcc	tggaaccga	ggattaatgg	gcaaaaagg	agaaattggg	1860
cctccaggac	agcaaggaaa	aaaaggagcc	ccagggatgc	ctggtttaata	gggaagcaat	1920
ggctcaccag	gccagcctgg	aacaccggga	tctaaggga	gcaaaggatga	acctggaatt	1980
caagggatgc	ctggggcttc	tgggctcaag	ggagaaccag	gagcaacggg	ttccccagga	2040
gaaccaggat	acatgggttt	acccgggatt	caaggaaaaa	agggggacaa	aggaaatcaa	2100
ggtgaaaaag	gtattcaggg	tcaaaaggga	gaaaatggaa	gacagggaat	tccagggcaa	2160

caggggaattc aaggccatca tgggtgcaaaa ggagagagag gtgaaaaggg agaacctggt	2220
gtccgaggtg ccattggatc aaaaggagaa tctgggggtgg atggcttgat ggggcccgcga	2280
ggctctaagg ggcaacctgg ggatccaggt cctcagggaac cccaggttt ggatgggaag	2340
cccggaagag agttttcaga acaatttatt cgacaagttt gcacagatgt aataagagcc	2400
cagctaccag tcttacttca gagtggaaga attagaaaatt gtgatcattg cctgtcccaa	2460
catggctccc cggttattcc tgggccacct ggtccgatag gccagagggg tcccagagga	2520
ttacctggtt tgccaggaag agatgggtgtt cctggattag tgggtgtccc tggacgtcca	2580
ggtgtcagag gattaaaagg cctaccagga agaaatgggg aaaaaggag ccaagggttt	2640
gggtatcctg gagaacaagg tcctcctggt ccccagggtc cagagggccc tcctggaata	2700
agcaaagaag gtcctccagg agaccaggt ctccctggca aagatggaga ccatggaaaa	2760
cctggaatcc aagggcaacc agggccccca ggcatctgcg acccatcact atgttttagt	2820
gtaattgccca gaagagatcc gttcagaaaa ggaccaaact attag	2865

<210> 6
 <211> 22
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer deduced from the clone 682J15

<400> 6	
ggttcacctt tgcttccctt ag	22

<210> 7
 <211> 23
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer, corresponding to nucleotides 1823-1845 in the hCOLA1 cDNA

<400> 7	
ttggcccatt aatcctcggt ttc	23

<210> 8
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> upstream primer

<400> 8	
attcctgggc cacctgggtcc gata	24

<210> 9
 <211> 21
 <212> DNA

<213> artificial sequence
 <220>
 <223> downstream primer
 <400> 9
 ctaatagttt ggtccttttc t 21

<210> 10
 <211> 26
 <212> DNA
 <213> artificial sequence
 <220>
 <223> primer, GAPDH
 <400> 10
 tgaaggtcgg agtcaacgga tttggt 26

<210> 11
 <211> 24
 <212> DNA
 <213> artificial sequence
 <220>
 <223> primer, GAPDH
 <400> 11
 catgtgggcc atgaggtcca ccac 24

<210> 12
 <211> 23
 <212> DNA
 <213> artificial sequence
 <220>
 <223> primer, hCOLA1 collagen
 <400> 12
 ttcctggaaa ccgaggatta atg 23

<210> 13
 <211> 22
 <212> DNA
 <213> artificial sequence
 <220>
 <223> primer, hCOLA1 collagen
 <400> 13
 agtccacgat cacccttgtc ac 22

<210> 14
 <211> 24
 <212> DNA
 <213> artificial sequence
 <220>
 <223> primer for the coding region

<400> 14
atggctcact atattacatt tctc

24

<210> 15
<211> 43
<212> DNA
<213> artificial sequence

<220>
<223> primer for the coding region

<400> 15
ttagtgatgg tgatggtgat gctcatagtt tggtcctttt ctg

43